#91508
5/11/02

PCT10

ENTERED

RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/10/009,178   TIME: 13:58:37

Input Set : A:\10009178.txt
Output Set: N:\CRF3\03132002\J009178.raw

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 3 <110> APPLICANT: OKAMOTO, Hiroshi
 5 <120> TITLE OF INVENTION: Reg-Binding Protein
 7 <130> FILE REFERENCE: 3914-4
 9 <140> CURRENT APPLICATION NUMBER: US 10/009,178
C--> 10 <141> CURRENT FILING DATE: 2002-02-15
12 <150> PRIOR APPLICATION NUMBER: PCT/JP00/03764
13 <151> PRIOR FILING DATE: 2000-06-09
15 <150> PRIOR APPLICATION NUMBER: JP 1999-164488
16 <151> PRIOR FILING DATE: 1999-06-10
18 <160> NUMBER OF SEQ ID NOS: 10
20 <170> SOFTWARE: MS Word
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1599
24 <212> TYPE: DNA
25 <213> ORGANISM: Rattus norvegicus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (168)..(1259)
31 <400> SEQUENCE: 1
32 tcagcgagga aaatgaaatt cccattttat ttggtgcctt gtgcagggag cacactgatc 60
34 cctctagaac cttgtgtgtg aaaaagaggt cgagttttgt caaacagact catggttatg 120
36 gcaagtgatc cgacgtgacc agagtgggca agagccacag tgaactc atg aca ggc   176
37                                                    Met Thr Gly
38                                                     1
40 tat acc atg ttg cgg aat ggg gga gtg ggg aac ggt ggt cag acc tgt 224
41 Tyr Thr Met Leu Arg Asn Gly Gly Val Gly Asn Gly Gly Gln Thr Cys
42         5                       10                  15
44 atg ctg cgc tgg tcc aac cgc atc cgg ctg acc tgg ctg agt ttc acg 272
45 Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu Ser Phe Thr
46  20                  25                  30                  35
48 ctg ttc atc atc ctg gtc ttc ttc ccc ctc att gcc cac tat tac ctc 320
49 Leu Phe Ile Ile Leu Val Phe Phe Pro Leu Ile Ala His Tyr Tyr Leu
50                  40                  45                  50
52 acc act ctg gat gag gca gat gag gcc ggc aag cgc atc ttt ggc ccc 368
53 Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile Phe Gly Pro
54          55                  60                  65
56 cgg gct ggc aac gag ctc tgt gag gta aag cac gtc cta gat ctt tgt 416
57 Arg Ala Gly Asn Glu Leu Cys Glu Val Lys His Val Leu Asp Leu Cys
58          70                  75                  80
60 cgg atc cgc gag tct gtg agc gaa gag ctt cta cag cta gaa gcc aag 464
61 Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln Leu Glu Ala Lys
62          85                  90                  95
64 cgg cag gag ctg aac agc gag att gcc aag cta aac ctc aag att gaa 512
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```
 65 Arg Gln Glu Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu Lys Ile Glu
 66 100               105               110               115
 68 gcc tgt aag aag agt ata gag aac gcc aag cag gac ctg ctg cag ctc    560
 69 Ala Cys Lys Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu Leu Gln Leu
 70               120               125               130
 72 aag aat gtc att agc cag aca gag cac tcc tac aag gag ctg atg gcc    608
 73 Lys Asn Val Ile Ser Gln Thr Glu His Ser Tyr Lys Glu Leu Met Ala
 74               135               140               145
 76 cag aac cag ccc aaa ctg tca ctg ccc atc cgg ctg ctc cct gag aag    656
 77 Gln Asn Gln Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu Pro Glu Lys
 78               150               155               160
 80 gat gac gct ggc ctt cca ccc ccc aag gtc act cgg ggt tgc cgg cta    704
 81 Asp Asp Ala Gly Leu Pro Pro Pro Lys Val Thr Arg Gly Cys Arg Leu
 82               165               170               175
 84 cac aac tgc ttc gat tac tct cgt tgc cct ctg acg tct ggc ttt cct    752
 85 His Asn Cys Phe Asp Tyr Ser Arg Cys Pro Leu Thr Ser Gly Phe Pro
 86 180               185               190               195
 88 gtc ttc gtc tat gac agt gac cag ttt gcc ttt ggg agc tac ctg gac    800
 89 Val Phe Val Tyr Asp Ser Asp Gln Phe Ala Phe Gly Ser Tyr Leu Asp
 90               200               205               210
 92 cct ttg gtc aag cag gct ttt cag gct aca gtg aga gcc aac gtt tat    848
 93 Pro Leu Val Lys Gln Ala Phe Gln Ala Thr Val Arg Ala Asn Val Tyr
 94               215               220               225
 96 gtt aca gaa aat gca gcc atc gcc tgc ctg tat gtg gtg tta gtg gga    896
 97 Val Thr Glu Asn Ala Ala Ile Ala Cys Leu Tyr Val Val Leu Val Gly
 98               230               235               240
100 gag ata caa gag ccc gct gtg ctg cag cct gcc gac ctt gag aag cag    944
101 Glu Ile Gln Glu Pro Ala Val Leu Gln Pro Ala Asp Leu Glu Lys Gln
102               245               250               255
104 ctg cat tct ctg cca cac tgg agg aca gac gga cac aac cat gtc atc    992
105 Leu His Ser Leu Pro His Trp Arg Thr Asp Gly His Asn His Val Ile
106 260               265               270               275
108 atc aat ctg tcc cgg aag tca gac aca caa aat tta ctg tac aat gtc    1040
109 Ile Asn Leu Ser Arg Lys Ser Asp Thr Gln Asn Leu Leu Tyr Asn Val
110               280               285               290
112 agt aca ggt cgg gcc atg gtg gcc cag tct acc ttc tat gct gcc cag    1088
113 Ser Thr Gly Arg Ala Met Val Ala Gln Ser Thr Phe Tyr Ala Ala Gln
114               295               300               305
116 tac aga gct ggc ttt gac ttg gtt gtg tca cca ctt gtc cat gcc atg    1136
117 Tyr Arg Ala Gly Phe Asp Leu Val Val Ser Pro Leu Val His Ala Met
118               310               315               320
120 tct gaa ccc aac ttc atg gaa atc cca cgt gta act att ttt tca ctt    1184
121 Ser Glu Pro Asn Phe Met Glu Ile Pro Arg Val Thr Ile Phe Ser Leu
122               325               330               335
124 ggg aga ggt gag gaa gaa caa gag aag ctg ggg gtg tgg aga ggc aga    1232
125 Gly Arg Gly Glu Glu Glu Gln Glu Lys Leu Gly Val Trp Arg Gly Arg
126 340               345               350               355
128 ccc ccc cca ggc tgg ggt gct ggc ccc tagactaggg tgctgacccc          1279
129 Pro Pro Pro Gly Trp Gly Ala Gly Pro
```

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```
130                  360
132 tgggctgggg tgctgcgtgc tacctcccac tgtgaaatcg atggtgctca caattgtctc 1339
134 ttgtaatgta tgtgattttt ttttaaggag aaaaagaaac tatttaagat tctgaaggtg 1399
136 ctactatttt tgttgccaca ggctttaaag aaactttctg agtgggtggg gccttgccca 1459
138 cttatctttc tctcctccaa atgaggagtt aaaaatgtta ctaaattgcc cgcacgtgta 1519
140 atccgctgaa aagaaaaaaa aaaaagaaaa aaaaaggaa ggaagaaggg aagaaggaa 1579
142 ggaaggaagg aaggaaagga                                        1599
```

145 <210> SEQ ID NO: 2
146 <211> LENGTH: 364
147 <212> TYPE: PRT
148 <213> ORGANISM: Rattus norvegicus
150 <400> SEQUENCE: 2

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151 Met Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Val Gly Asn Gly Gly
152  1               5                  10                  15
154 Gln Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu
155             20                  25                  30
157 Ser Phe Thr Leu Phe Ile Ile Leu Val Phe Phe Pro Leu Ile Ala His
158             35                  40                  45
160 Tyr Tyr Leu Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile
161      50                  55                  60
163 Phe Gly Pro Arg Ala Gly Asn Glu Leu Cys Glu Val Lys His Val Leu
164  65                  70                  75                  80
166 Asp Leu Cys Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln Leu
167             85                  90                  95
169 Glu Ala Lys Arg Gln Glu Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu
170             100                 105                 110
172 Lys Ile Glu Ala Cys Lys Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu
173             115                 120                 125
175 Leu Gln Leu Lys Asn Val Ile Ser Gln Thr Glu His Ser Tyr Lys Glu
176      130                 135                 140
178 Leu Met Ala Gln Asn Gln Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu
179 145                 150                 155                 160
181 Pro Glu Lys Asp Asp Ala Gly Leu Pro Pro Pro Lys Val Thr Arg Gly
182             165                 170                 175
184 Cys Arg Leu His Asn Cys Phe Asp Tyr Ser Arg Cys Pro Leu Thr Ser
185                 180                 185                 190
187 Gly Phe Pro Val Phe Val Tyr Asp Ser Asp Gln Phe Ala Phe Gly Ser
188          195                 200                 205
190 Tyr Leu Asp Pro Leu Val Lys Gln Ala Phe Gln Ala Thr Val Arg Ala
191      210                 215                 220
193 Asn Val Tyr Val Thr Glu Asn Ala Ala Ile Ala Cys Leu Tyr Val Val
194 225                 230                 235                 240
196 Leu Val Gly Glu Ile Gln Glu Pro Ala Val Leu Gln Pro Ala Asp Leu
197             245                 250                 255
199 Glu Lys Gln Leu His Ser Leu Pro His Trp Arg Thr Asp Gly His Asn
200             260                 265                 270
202 His Val Ile Ile Asn Leu Ser Arg Lys Ser Asp Thr Gln Asn Leu Leu
203      275                 280                 285
205 Tyr Asn Val Ser Thr Gly Arg Ala Met Val Ala Gln Ser Thr Phe Tyr
```

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PATENT APPLICATION: US/10/009,178   TIME: 13:58:37

Input Set : A:\10009178.txt
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```
206     290                  295                  300
208 Ala Ala Gln Tyr Arg Ala Gly Phe Asp Leu Val Val Ser Pro Leu Val
209 305                  310                  315                  320
211 His Ala Met Ser Glu Pro Asn Phe Met Glu Ile Pro Arg Val Thr Ile
212                  325                  330                  335
214 Phe Ser Leu Gly Arg Gly Glu Glu Glu Gln Glu Lys Leu Gly Val Trp
215                  340                  345                  350
217 Arg Gly Arg Pro Pro Pro Gly Trp Gly Ala Gly Pro
218         355                  360
221 <210> SEQ ID NO: 3
222 <211> LENGTH: 3198
223 <212> TYPE: DNA
224 <213> ORGANISM: Rattus norvegicus
226 <220> FEATURE:
227 <221> NAME/KEY: CDS
228 <222> LOCATION: (5)..(2761)
230 <400> SEQUENCE: 3
231 actc atg aca ggc tat acc atg ttg cgg aat ggg gga gtg ggg aac ggt   49
232      Met Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Val Gly Asn Gly
233       1              5                  10                  15
235 ggt cag acc tgt atg ctg cgc tgg tcc aac cgc atc cgg ctg acc tgg   97
236 Gly Gln Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp
237              20                  25                  30
239 ctg agt ttc acg ctg ttc atc atc ctg gtc ttc ttc ccc ctc att gcc  145
240 Leu Ser Phe Thr Leu Phe Ile Ile Leu Val Phe Phe Pro Leu Ile Ala
241              35                  40                  45
243 cac tat tac ctc acc act ctg gat gag gca gat gag gcc ggc aag cgc  193
244 His Tyr Tyr Leu Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg
245          50                  55                  60
247 atc ttt ggc ccc cgg gct ggc aac gag ctc tgt gag gta aag cac gtc  241
248 Ile Phe Gly Pro Arg Ala Gly Asn Glu Leu Cys Glu Val Lys His Val
249      65                  70                  75
251 cta gat ctt tgt cgg atc cgc gag tct gtg agc gaa gag ctt cta cag  289
252 Leu Asp Leu Cys Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln
253 80                  85                  90                  95
255 cta gaa gcc aag cgg cag gag ctg aac agc gag att gcc aag cta aac  337
256 Leu Glu Ala Lys Arg Gln Glu Leu Asn Ser Glu Ile Ala Lys Leu Asn
257              100                 105                 110
259 ctc aag att gaa gcc tgt aag aag agt ata gag aac gcc aag cag gac  385
260 Leu Lys Ile Glu Ala Cys Lys Lys Ser Ile Glu Asn Ala Lys Gln Asp
261              115                 120                 125
263 ctg ctg cag ctc aag aat gtc att agc cag aca gag cac tcc tac aag  433
264 Leu Leu Gln Leu Lys Asn Val Ile Ser Gln Thr Glu His Ser Tyr Lys
265          130                 135                 140
267 gag ctg atg gcc cag aac cag ccc aaa ctg tca ctg ccc atc cgg ctg  481
268 Glu Leu Met Ala Gln Asn Gln Pro Lys Leu Ser Leu Pro Ile Arg Leu
269      145                 150                 155
271 ctc cct gag aag gat gac gct ggc ctt cca ccc ccc aag gtc act cgg  529
272 Leu Pro Glu Lys Asp Asp Ala Gly Leu Pro Pro Pro Lys Val Thr Arg
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```
273 160                      165                  170                      175
275 ggt tgc cgg cta cac aac tgc ttc gat tac tct cgt tgc cct ctg acg    577
276 Gly Cys Arg Leu His Asn Cys Phe Asp Tyr Ser Arg Cys Pro Leu Thr
277                      180                  185                  190
279 tct ggc ttt cct gtc ttc gtc tat gac agt gac cag ttt gcc ttt ggg    625
280 Ser Gly Phe Pro Val Phe Val Tyr Asp Ser Asp Gln Phe Ala Phe Gly
281                      195                  200                  205
283 agc tac ctg gac cct ttg gtc aag cag gct ttt cag gct aca gtg aga    673
284 Ser Tyr Leu Asp Pro Leu Val Lys Gln Ala Phe Gln Ala Thr Val Arg
285           210                  215                  220
287 gcc aac gtt tat gtt aca gaa aat gca gcc atc gcc tgc ctg tat gtg    721
288 Ala Asn Val Tyr Val Thr Glu Asn Ala Ala Ile Ala Cys Leu Tyr Val
289           225                  230                  235
291 gtg tta gtg gga gag ata caa gag ccc gct gtg ctg cag cct gcc gac    769
292 Val Leu Val Gly Glu Ile Gln Glu Pro Ala Val Leu Gln Pro Ala Asp
293 240                  245                  250                  255
295 ctt gag aag cag ctg cat tct ctg cca cac tgg agg aca gac gga cac    817
296 Leu Glu Lys Gln Leu His Ser Leu Pro His Trp Arg Thr Asp Gly His
297                      260                  265                  270
299 aac cat gtc atc atc aat ctg tcc cgg aag tca gac aca caa aat tta    865
300 Asn His Val Ile Ile Asn Leu Ser Arg Lys Ser Asp Thr Gln Asn Leu
301                      275                  280                  285
303 ctg tac aat gtc agt aca ggt cgg gcc atg gtg gcc cag tct acc ttc    913
304 Leu Tyr Asn Val Ser Thr Gly Arg Ala Met Val Ala Gln Ser Thr Phe
305           290                  295                  300
307 tat gct gcc cag tac aga gct ggc ttt gac ttg gtt gtg tca cca ctt    961
308 Tyr Ala Ala Gln Tyr Arg Ala Gly Phe Asp Leu Val Val Ser Pro Leu
309           305                  310                  315
311 gtc cat gcc atg tct gaa ccc aac ttc atg gaa atc cca ccg cag gtg    1009
312 Val His Ala Met Ser Glu Pro Asn Phe Met Glu Ile Pro Pro Gln Val
313 320                  325                  330                  335
315 cca gtt aag cgg aaa tat ctc ttc act ttc cag ggt gag aag att gag    1057
316 Pro Val Lys Arg Lys Tyr Leu Phe Thr Phe Gln Gly Glu Lys Ile Glu
317                      340                  345                  350
319 tct cta aga tct agc ctt cag gag gcc cgt tcc ttt gag gaa gaa atg    1105
320 Ser Leu Arg Ser Ser Leu Gln Glu Ala Arg Ser Phe Glu Glu Glu Met
321           355                  360                  365
323 gag ggt gac cct ccg gcc gac tat gat gat cga atc att gcc acc ctc    1153
324 Glu Gly Asp Pro Pro Ala Asp Tyr Asp Asp Arg Ile Ile Ala Thr Leu
325           370                  375                  380
327 aag gcc gta cag gac agc aag cta gat cag gtg ctg gta gaa ttt act    1201
328 Lys Ala Val Gln Asp Ser Lys Leu Asp Gln Val Leu Val Glu Phe Thr
329           385                  390                  395
331 tgc aaa aac cag cca aag ccc agt ctg cct act gag tgg gca ctg tgt    1249
332 Cys Lys Asn Gln Pro Lys Pro Ser Leu Pro Thr Glu Trp Ala Leu Cys
333 400                  405                  410                  415
335 ggg gag cgg gag gac cgg cta gag tta ctg aag ctc tcc acc ttc gcc    1297
336 Gly Glu Arg Glu Asp Arg Leu Glu Leu Leu Lys Leu Ser Thr Phe Ala
337                      420                  425                  430
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VERIFICATION SUMMARY   DATE: 03/13/2002
PATENT APPLICATION: US/10/009,178   TIME: 13:58:38

Input Set : A:\10009178.txt
Output Set: N:\CRF3\03132002\J009178.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date